

# Xinmeng Li

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## Education

Tufts University	<b>Ph.D. in Computer Science</b> Research Focus on Computational Biology and Machine learning	<i>Expected May 2021</i>
Tufts University	<b>M.S. in Computer Science</b> (GPA 3.9/4.0)	<i>2015 - 2017</i>
Sichuan University	<b>B.S. in Computer Science</b> (Excellent Graduate, top 2%)	<i>2011 - 2015</i>

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## Professional Experience

Research Assistant	<b>Tufts University</b> • Perform research in the area of computational biology and machine learning. • Mentor and train undergraduate students on research. • Publish research finding in journals and conferences.	<i>2016 - present</i>
Teaching Assistant	<b>Tufts University</b> • Prepare materials for courses in machine learning and computational biology. • Manage lab operations and hold office hour to supervise students.	<i>2015 - present</i>
Summer Intern	<b>Food and Drug Administration</b> • Develop deep learning models to assist drug review computationally. • Analyze data of drug concentration over time in plasma with models.	<i>2019</i>

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## Research Projects

Reaction Prediction	One-class Recommender Systems for Modeling Enzyme-substrate Interactions • Construct recommender systems to predict enzyme-substrate interactions. • Evaluate performance of SVD-based and neural network-based models. • Solve the one-class classification problem with metabolomic data.
Sequence Design	Antibody Sequence Analysis Pipeline using Statistical Testing and Machine Learning • Develop a pipeline to analyze salient features in antibody protein sequences. • Provide antibody sequence design recommendations on salient features. • Make the pipeline available at <a href="http://github.com/HassounLab/ASAP-SML">http://github.com/HassounLab/ASAP-SML</a> .
Metabolite Annotation	Metabolite Annotation with Tandem Mass Spectra Data using Deep Learning • Identify metabolites with spectra data using deep learning models. • Analyze metabolite structure representation data and tandem mass spectra data.
Pathway Annotation	Pathway Annotation in Metabolic Network with Metabolomics Data • Annotation active pathways based on statistical tests and clustering methods. • Analyze untargeted metabolomics data in metabolomic networks.

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## Awards

Scholarships	Tang Lixin Scholarship, Tang Lixin Education Foundation Grace Hopper Conference Scholarship, AnitaB.org CRA-W Conference Scholarship, Computing Research Association Kerk and Janelle Loevner Graduate Fellowship, Tufts University	<i>2014 - present</i> <i>2019</i> <i>2018</i> <i>2017</i>
Research Grants	College Student Innovative Research Grant, Ministry of Education of China Student Research Grant, Sichuan University	<i>2013</i> <i>2012</i>

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## Programming Skills

Languages	Proficient in Python, MATLAB, C++, LaTeX
Python Packages	Familiar with Numpy, Pandas, RdKit, TensorFlow, PyTorch, Keras
Biochem Databases	Experienced with PDB, PubChem, KEGG, IMG, HMDB

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## Publications

Journal Papers	<ul style="list-style-type: none"><li>• <b>Li X</b>, Van Deventer JA, Hassoun S. "ASAP-SML: An Antibody Sequence Analysis Pipeline using Statistical Testing and Machine Learning." PLoS computational biology. 16.4 (2020).</li><li>• Hu R, Wang Y, Yang M, <b>Li X</b>, Luo Z, Li G. "Improved Analysis of Inorganic Coal Properties Based on Near-infrared Reflectance Spectroscopy." Analytical Methods. 7 (2015)</li></ul>
Conference Posters	<ul style="list-style-type: none"><li>• <b>Li X</b>, Liu L, Hassoun S. "One-class Recommender Systems for Modeling Enzyme-substrate Interactions." ISCB International Conference on Intelligent Systems for Molecular Biology, 2020.</li><li>• <b>Li X</b>, Van Deventer JA, Hassoun S. "ASAP-SML: An Antibody Sequence Analysis Pipeline using Statistical Testing and Machine Learning." ISCB International Conference on Intelligent Systems for Molecular Biology, 2020.</li><li>• <b>Li X</b>, Van Deventer JA, Hassoun S. "Towards the Design of Matrix Metalloproteinases (MMP) Antibody Sequences." ACM International Conference on Bioinformatics, 2017.</li><li>• Porokhin V, <b>Li X</b>, Hassoun S. "Pathway Enrichment Analysis for Untargeted Metabolomics." ACM International Conference on Bioinformatics, 2017.</li></ul>
Software Copyright	<ul style="list-style-type: none"><li>• <b>Li X</b>, Liu L. "Volume Measurement System of Massive Material Based on Aerial Photography." Chinese Software Copyright, No.2014SR096344.</li></ul>